16075 4

Schreiber, David

From:	Steadman, David (AU1652)
Sent:	Tuesday, July 12, 2005 12:29 PM
To:	Schreiber, David
Subject:	10/600,751 sequence search request

NAME: David Steadman
AU: 1656
Date:07/12/05
Office: Remsen 2B05
Mailbox: Remsen 3C70

Please perform the following search or searches in commercial and interference databases:

1) Standard search of SEQ ID NO:6 against amino acid databases.

2) Standard search of SEQ ID NO:9 against amino acid databases.

Please save results to diskette.

Thank you very much.

David J. Steadman, Ph.D.
Primary Examiner
Art Unit 1656
Protein Crystallography and Recombinant Enzymes
Office: Remsen 2B05
Mailbox: Remsen 3C70
Phone: (571) 272-0942

1

OM protein - protein search, using sw model

Run on: July 12, 2005, 15:06:28 ; Search time 223.808 Seconds
                                           (without alignments)
                                           444.119 Million cell updates/sec

Title: US-10-600-751-6
Perfect score: 1340
Sequence: 1 VPATLPQLTPTLVSLLEVIE..........TNQIPKYSNGNIKKLLFHQK 257

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
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                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1340	100.0	257	8	ADH26660	Adh26660 Human wil
2	1340	100.0	777	1	AAP80919	Aap80919 Sequence
3	1340	100.0	777	2	AAY21623	Aay21623 Ligand bi
4	1340	100.0	777	6	ABU08023	Abu08023 Wild-type
5	1340	100.0	777	6	ABR44285	Abr44285 Human GRa
6	1340	100.0	777	7	ADE57452	Ade57452 Human Pro
7	1340	100.0	777	7	ADF30368	Adf30368 Human ful
8	1340	100.0	777	7	ADG10636	Adg10636 Human STA
9	1340	100.0	777	7	ADF73070	Adf73070 Glucocort
10	1340	100.0	777	8	ADH26656	Adh26656 Human wil
11	1340	100.0	777	8	ADH67937	Adh67937 Human glu
12	1340	100.0	777	8	ADP05673	Adp05673 Human nuc
13	1340	100.0	777	8	ADS88247	Ads88247 Human pro
14	1340	100.0	777	8	ADQ39890	Adq39890 Human myo
15	1340	100.0	777	8	ADQ39891	Adq39891 Human myo
16	1340	100.0	781	6	ABR41246	Abr41246 Human DIT
17	1340	100.0	1003	6	ABP58320	Abp58320 Glucocort
18	1338	99.9	257	6	ABU08045	Abu08045 Mutant hu
19	1336	99.7	257	6	ABU08044	Abu08044 Mutant hu
20	1335	99.6	257	6	ABU08043	Abu08043 Mutant hu
21	1335	99.6	667	2	AAW44701	Aaw44701 Chimeric
22	1335	99.6	777	2	AAW44700	Aaw44700 Mutant nu
23	1333	99.5	257	6	ABU08042	Abu08042 Mutant hu
24	1332	99.4	257	8	ADH26662	Adh26662 Human mut

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25    1332    99.4    777    6    ABU08024              Abu08024 Mutant hu
26    1332    99.4    777    8    ADH26658              Adh26658 Human mut
27    1331    99.3    257    6    ABU08049              Abu08049 Mutant hu
28    1331    99.3    777    6    ABU08025              Abu08025 Mutant hu
29    1330    99.3    257    6    ABU08046              Abu08046 Mutant hu
30    1329    99.2    255    8    ADI29487              Adi29487 Human lig
31    1329    99.2    483    6    ABP58319              Abp58319 Glucocort
32    1328    99.1    777    7    ADF73072              Adf73072 Glucocort
33    1327    99.0    257    6    ABU08047              Abu08047 Mutant hu
34    1327    99.0    257    6    ABU08048              Abu08048 Mutant hu
35    1326    99.0    257    6    ABU08041              Abu08041 Mutant hu
36    1323    98.7    276    7    ADF30365              Adf30365 Human glu
37    1320    98.5    277    7    ADF30366              Adf30366 Human glu
38    1318    98.4    613    4    AAB47153              Aab47153 iCre-FRT-
39    1308    97.6    797    7    ADF73074              Adf73074 Glucocort
40    1304    97.3    251    3    AAB26787              Aab26787 Glucocort
41    1291    96.3    739    8    ADH67939              Adh67939 Mouse glu
42    1291    96.3    783    8    ADH67952              Adh67952 Mouse glu
43    1291    96.3    783    8    ADP05675              Adp05675 Mouse nuc
44    1284    95.8    284    3    AAB19249              Aab19249 A rat glu
45    1284    95.8    795    7    ADE57450              Ade57450 Rat Prote
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OM protein - protein search, using sw model

Run on: July 12, 2005, 15:09:14 ; Search time 56.9004 Seconds
                                          (without alignments)
                                          337.165 Million cell updates/sec

Title: US-10-600-751-6
Perfect score: 1340
Sequence: 1 VPATLPQLTPTLVSLLEVIE..........TNQIPKYSNGNIKKLLFHQK 257

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
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                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                              SUMMARIES

          %
Result   Query
  No.   Score Match Length DB ID   Description
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     2   1340 100.0   777 3 US-08-980-115-13   Sequence 13, Appl
     3   1335   99.6   667 4 US-09-125-491C-4   Sequence 4, Appli
     4   1335   99.6   777 4 US-09-125-491C-2   Sequence 2, Appli
     5 1291.5   96.4   356 6 5223606-7   Patent No. 5223606
     6 1291.5   96.4   356 6 5223606-7   Patent No. 5223606
     7   1284   95.8   284 2 US-08-592-214A-24   Sequence 24, Appl
     8   1284   95.8   284 3 US-09-149-976-24   Sequence 24, Appl
     9   1284   95.8   795 1 US-07-716-827C-5   Sequence 5, Appli
    10   1276   95.2   284 3 US-08-659-188-20   Sequence 20, Appl
    11   1276   95.2   284 3 US-08-655-227-20   Sequence 20, Appl
    12   1276   95.2   284 3 US-08-655-241-20   Sequence 20, Appl
    13   1276   95.2   284 3 US-09-398-326-20   Sequence 20, Appl
    14   1276   95.2   284 4 US-09-853-450-20   Sequence 20, Appl
    15   1272   94.9   1070 4 US-09-091-042A-2   Sequence 2, Appli
    16   1254   93.6   534 3 US-08-875-223-8   Sequence 8, Appli
    17   773   57.7   984 3 US-08-764-870-15   Sequence 15, Appl
    18   773   57.7   984 3 US-08-980-115-15   Sequence 15, Appl
    19   773   57.7   984 4 US-09-976-594-127   Sequence 127, App
    20 731.5   54.6   363 6 5223606-6   Patent No. 5223606
    21 731.5   54.6   363 6 5223606-6   Patent No. 5223606
    22 729.5   54.4   933 3 US-08-764-870-14   Sequence 14, Appl
    23 729.5   54.4   933 3 US-08-980-115-14   Sequence 14, Appl
    24 729.5   54.4   990 4 US-09-949-016-10562   Sequence 10562, A
    25 724.5   54.1   255 4 US-09-687-609A-2   Sequence 2, Appli
    26 662.5   49.4   260 4 US-09-687-609A-1   Sequence 1, Appli

27	662.5	49.4	452	3	US-08-764-870-16	Sequence 16, Appl
28	662.5	49.4	452	3	US-08-980-115-16	Sequence 16, Appl
29	662.5	49.4	918	3	US-09-041-886-11	Sequence 11, Appl
30	662.5	49.4	919	4	US-09-538-092-895	Sequence 895, App
31	662.5	49.4	923	4	US-09-497-822C-19	Sequence 19, Appl
32	643.5	48.0	996	4	US-09-497-822C-21	Sequence 21, Appl
33	512	38.2	98	4	US-09-652-345-4	Sequence 4, Appli
34	341	25.4	98	4	US-09-652-345-3	Sequence 3, Appli
35	323	24.1	60	5	PCT-US94-14074-1	Sequence 1, Appli
36	240.5	17.9	596	2	US-08-836-620A-16	Sequence 16, Appl
37	238	17.8	264	4	US-09-660-979-1	Sequence 1, Appli
38	236.5	17.6	595	4	US-10-052-092-30	Sequence 30, Appl
39	235.5	17.6	701	4	US-10-052-092-12	Sequence 12, Appl
40	235	17.5	595	3	US-08-764-870-12	Sequence 12, Appl
41	235	17.5	595	3	US-08-980-115-12	Sequence 12, Appl
42	233.5	17.4	595	4	US-10-052-092-31	Sequence 31, Appl
43	233	17.4	547	4	US-10-052-092-10	Sequence 10, Appl
44	233	17.4	591	2	US-08-836-620A-17	Sequence 17, Appl
45	233	17.4	595	3	US-09-041-886-35	Sequence 35, Appl

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OM protein - protein search, using sw model

Run on: July 12, 2005, 15:16:10 ; Search time 204.841 Seconds
                                          (without alignments)
                                          484.703 Million cell updates/sec

Title: US-10-600-751-6
Perfect score: 1340
Sequence: 1 VPATLPQLTPTLVSLLEVIE.........TNQIPKYSNGNIKKLLFHQK 257

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1726218 seqs, 386331768 residues

Total number of hits satisfying chosen parameters: 1726218

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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                 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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                 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
                 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
                 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
                 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
                 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

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2	1340	100.0	777	14	US-10-153-668-226	Sequence 226, App
3	1340	100.0	777	16	US-10-661-217-2	Sequence 2, Appli
4	1340	100.0	777	16	US-10-661-217-4	Sequence 4, Appli
5	1340	100.0	777	17	US-10-741-600-1553	Sequence 1553, Ap
6	1340	100.0	777	17	US-10-741-600-1554	Sequence 1554, Ap
7	1340	100.0	1003	14	US-10-151-133-2	Sequence 2, Appli
8	1329	99.9	483	14	US-10-151-133-1	Sequence 1, Appli
9	1276	95.2	284	9	US-09-853-450-20	Sequence 20, Appl
10	1276	95.2	284	16	US-10-794-923-20	Sequence 20, Appl

11	1272	94.9	1070	14	US-10-001-486B-2	Sequence 2, Appli
12	1081	80.7	742	9	US-09-308-295-2	Sequence 2, Appli
13	1081	80.7	742	16	US-10-755-889-550	Sequence 550, App
14	773	57.7	984	15	US-10-087-080-36	Sequence 36, Appl
15	729.5	54.4	258	14	US-10-220-981-3	Sequence 3, Appli
16	729.5	54.4	314	9	US-09-887-280-4	Sequence 4, Appli
17	729.5	54.4	381	16	US-10-416-708A-56	Sequence 56, Appl
18	729.5	54.4	933	14	US-10-207-655-63	Sequence 63, Appl
19	729.5	54.4	933	15	US-10-332-176A-4	Sequence 4, Appli
20	724.5	54.1	251	16	US-10-469-866-16	Sequence 16, Appl
21	724.5	54.1	255	16	US-10-878-851-2	Sequence 2, Appli
22	695.5	51.9	240	9	US-09-905-176-13	Sequence 13, Appl
23	684.5	51.1	630	15	US-10-400-053-15	Sequence 15, Appl
24	684.5	51.1	654	15	US-10-400-053-14	Sequence 14, Appl
25	682.5	50.9	630	15	US-10-400-053-24	Sequence 24, Appl
26	678.5	50.6	574	15	US-10-332-176A-6	Sequence 6, Appli
27	678.5	50.6	574	15	US-10-332-176A-8	Sequence 8, Appli
28	678.5	50.6	599	15	US-10-332-176A-10	Sequence 10, Appl
29	669.5	50.0	689	14	US-10-202-846-2	Sequence 2, Appli
30	662.5	49.4	260	16	US-10-878-851-1	Sequence 1, Appli
31	662.5	49.4	263	14	US-10-220-981-1	Sequence 1, Appli
32	662.5	49.4	388	9	US-09-997-267-2	Sequence 2, Appli
33	662.5	49.4	895	16	US-10-476-724A-2	Sequence 2, Appli
34	662.5	49.4	895	16	US-10-476-724A-4	Sequence 4, Appli
35	662.5	49.4	899	16	US-10-484-950-4	Sequence 4, Appli
36	662.5	49.4	899	16	US-10-484-950-6	Sequence 6, Appli
37	662.5	49.4	899	16	US-10-484-950-8	Sequence 8, Appli
38	662.5	49.4	902	17	US-10-886-384-21	Sequence 21, Appl
39	662.5	49.4	907	13	US-10-008-739A-2	Sequence 2, Appli
40	662.5	49.4	918	15	US-10-375-592A-3	Sequence 3, Appli
41	662.5	49.4	919	14	US-10-205-823-36	Sequence 36, Appl
42	662.5	49.4	919	15	US-10-058-270A-94	Sequence 94, Appl
43	662.5	49.4	919	16	US-10-333-894A-21	Sequence 21, Appl
44	662.5	49.4	923	17	US-10-886-384-19	Sequence 19, Appl
45	654.5	48.8	906	15	US-10-375-592A-4	Sequence 4, Appli

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OM protein - protein search, using sw model

Run on: July 12, 2005, 15:08:54 ; Search time 45.5203 Seconds
                                           (without alignments)
                                           543.224 Million cell updates/sec

Title: US-10-600-751-6
Perfect score: 1340
Sequence: 1 VPATLPQLTPTLVSLLEVIE..........TNQIPKYSNGNIKKLLFHQK 257

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_79:*
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                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score   Match Length DB   ID   Description
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     2   1291   96.3   783   1   A25691   glucocorticoid rec
     3   1284   95.8   795   1   QRRTG   glucocorticoid rec
     4   1233   92.0   771   2   A54273   glucocorticoid rec
     5   1081   80.7   742   1   QRHUGB   glucocorticoid rec
     6   1072   80.0   776   1   S44047   glucocorticoid rec
     7   1011   75.4   758   2   S60586   glucocorticoid rec
     8   773   57.7   984   2   A29513   mineralocorticoid
     9   762   56.9   981   2   A41401   mineralocorticoid
    10   732.5   54.7   923   2   A39596   progesterone recep
    11   731.5   54.6   930   2   A25923   progesterone recep
    12   729.5   54.4   933   1   QRHUP   progesterone recep
    13   727.5   54.3   923   2   I53280   progesterone recep
    14   723.5   54.0   786   2   A35466   progesterone recep
    15   662.5   49.4   899   2   A35895   androgen receptor
    16   662.5   49.4   902   2   B40494   androgen receptor
    17   662.5   49.4   919   2   A39248   androgen receptor
    18   654.5   48.8   910   2   A34721   androgen receptor
    19   631.5   47.1   344   2   I51330   androgen receptor
    20   623   46.5   911   2   B34721   androgen receptor
    21   612.5   45.7   848   2   JG0194   androgen receptor
    22   291.5   21.8   110   2   I53287   progesterone recep
    23   240.5   17.9   600   1   QRRTE   estrogen receptor
    24   239.5   17.9   599   1   QRMSE   estrogen receptor
    25   235.5   17.6   701   2   S64737   80K estrogen recep
    26   233.5   17.4   595   2   I47140   estradiol receptor
    27   233   17.4   595   1   QRHUE   estrogen receptor
    28   230.5   17.2   166   2   S35795   androgen receptor

29	230.5	17.2	589	1	QRCHE	estrogen receptor
30	227.5	17.0	433	2	B29345	steroid hormone re
31	221.5	16.5	521	2	A29345	steroid hormone re
32	215.5	16.1	433	2	S58087	estrogen receptor
33	214.5	16.0	477	2	S71400	estrogen receptor
34	214.5	16.0	530	2	JC5939	estrogen receptor
35	214	16.0	586	1	QRXLE	estrogen receptor
36	207.5	15.5	503	2	JW0046	estrogen receptor
37	188.5	14.1	620	2	T10423	estrogen receptor
38	187	14.0	535	2	S58224	oestrogen receptor
39	177	13.2	462	2	S44490	RXR type hormone r
40	173.5	12.9	574	2	A37197	estrogen receptor
41	165.5	12.4	536	2	A56590	ecdysteroid recept
42	145.5	10.9	878	2	A41055	ecdysone receptor
43	144.5	10.8	808	1	S33708	nuclear steroid/th
44	135	10.1	385	2	I53158	orphan nuclear rec
45	135	10.1	441	2	I50515	retinoid X recepto

OM protein - protein search, using sw model

Run on: July 12, 2005, 15:07:23 ; Search time 212.428 Seconds
                                          (without alignments)
                                          619.524 Million cell updates/sec

Title: US-10-600-751-6
Perfect score: 1340
Sequence: 1 VPATLPQLTPTLVSLLEVIE..........TNQIPKYSNGNIKKLLFHQK 257

Scoring table: BLOSUM62
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Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_03:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1340	100.0	777	1	GCR_HUMAN	P04150 homo sapien
2	1340	100.0	777	2	Q6N0A4	Q6n0a4 homo sapien
3	1329	99.2	777	1	GCR_AOTNA	P79686 aotus nancy
4	1329	99.2	777	1	GCR_SAIBB	O13186 saimiri bol
5	1329	99.2	777	2	Q6XLJ0	Q6xlj0 callithrix
6	1329	99.2	778	1	GCR_SAISC	O46567 saimiri sci
7	1326	99.0	777	1	GCR_SAGOE	P79269 saguinus oe
8	1298	96.9	583	2	Q865Y6	Q865y6 bos taurus
9	1291	96.3	783	1	GCR_MOUSE	P06537 mus musculu
10	1289	96.2	772	1	GCR_RABIT	P59667 oryctolagus
11	1284	95.8	795	1	GCR_RAT	P06536 rattus norv
12	1268	94.6	776	1	GCR_TUPGB	Q95267 tupaia glis
13	1233	92.0	771	1	GCR_CAVPO	P49115 cavia porce
14	1149	85.7	711	1	GCR_PIG	Q9nlu3 sus scrofa
15	1072	80.0	776	1	GCR_XENLA	P49844 xenopus lae
16	1072	80.0	776	2	Q6DDL0	Q6ddl0 xenopus lae
17	1034	77.2	669	2	Q6RKQ3	Q6rkq3 oncorhynchu
18	1025	76.5	793	2	Q8JJ91	Q8jj91 haplochromi
19	1025	76.5	802	2	Q8JJ90	Q8jj90 haplochromi
20	1024	76.4	807	1	GCR_PAROL	O73673 paralichthy
21	1022	76.3	779	2	Q8JJ92	Q8jj92 haplochromi
22	1019	76.0	818	2	Q6QB13	Q6qb13 dicentrarch
23	1011	75.4	758	1	GCR_ONCMY	P49843 oncorhynchu
24	794.5	59.3	779	2	Q6IVJ3	Q6ivj3 dicentrarch
25	773	57.7	984	1	MCR_HUMAN	P08235 homo sapien
26	769	57.4	982	1	MCR_SAISC	Q9n0w8 saimiri sci
27	769	57.4	983	2	Q6XLI9	Q6xli9 callithrix
28	769	57.4	987	2	Q6XLI8	Q6xli8 callithrix
29	762	56.9	981	1	MCR_RAT	P22199 rattus norv
30	761	56.8	978	1	MCR_MOUSE	Q8vii8 mus musculu

31	753.5	56.2	612	1	MCR_XENLA	Q91573 xenopus lae
32	753.5	56.2	979	2	Q66J29	Q66j29 xenopus lae
33	740.5	55.3	993	2	Q8JJ89	Q8jj89 haplochromi
34	738	55.1	977	1	MCR_TUPGB	Q29131 tupaia glis
35	736.5	55.0	583	2	Q9DEV4	Q9dev4 xenopus lae
36	736.5	55.0	703	2	Q8UVY3	Q8uvy3 xenopus lae
37	735.5	54.9	732	2	Q9DDU9	Q9ddu9 xenopus lae
38	732.5	54.7	698	2	Q8BW69	Q8bw69 mus musculu
39	732.5	54.7	923	1	PRGR_MOUSE	Q00175 mus musculu
40	731.5	54.6	482	2	Q690N0	Q690n0 bos taurus
41	731.5	54.6	930	1	PRGR_RABIT	P06186 oryctolagus
42	730.5	54.5	939	1	PRGR_CANFA	Q9glw0 canis famil
43	729.5	54.4	933	1	PRGR_HUMAN	P06401 homo sapien
44	727.5	54.3	923	1	PRGR_RAT	Q63449 rattus norv
45	723.5	54.0	786	1	PRGR_CHICK	P07812 gallus gall

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OM protein - protein search, using sw model

Run on: July 12, 2005, 15:06:28 ; Search time 12.1919 Seconds
                                           (without alignments)
                                           444.119 Million cell updates/sec

Title: US-10-600-751-9
Perfect score: 71
Sequence: 1 KENALLRYLLDKDD 14

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_16Dec04:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                             SUMMARIES
                  %
Result   Query
  No.   Score   Match Length DB   ID   Description
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     1   71   100.0   14   8 ADH26663   Adh26663 Human TIF
     2   71   100.0   19   5 AAU86409   Aau86409 Oestrogen
     3   71   100.0   19   8 ADM79120   Adm79120 Oestrogen
     4   71   100.0   20   7 ADG17808   Adg17808 Binding a
     5   71   100.0   20   8 ADJ92851   Adj92851 Co-activa
     6   71   100.0   25   3 AAY99871   Aay99871 Human nuc
     7   71   100.0   25   3 AAB13527   Aab13527 Farnesoid
     8   71   100.0   25   4 AAE12667   Aae12667 Biotinyla
     9   71   100.0   25   5 AAU84221   Aau84221 Molecular
    10   71   100.0   25   6 ABU08031   Abu08031 Nuclear r
    11   71   100.0   31   3 AAY58284   Aay58284 Human p16
    12   71   100.0   31   3 AAY58290   Aay58290 Human p16
    13   71   100.0   31   3 AAY58287   Aay58287 Human p16
    14   71   100.0   31   5 AAO20842   Aao20842 p160 coac
    15   71   100.0   31   5 AAO20840   Aao20840 p160 coac
    16   71   100.0   31   5 AAO20841   Aao20841 p160 coac
    17   71   100.0   133   5 AAE16444   Aae16444 GRIP pept
    18   71   100.0   248   8 ADM93125   Adm93125 Human lig
    19   71   100.0   730   8 ADM93130   Adm93130 Human fus
    20   71   100.0   1263   6 AAE36002   Aae36002 Human TIF
    21   71   100.0   1263   6 ABR43917   Abr43917 Human TIF
    22   71   100.0   1263   8 ADN12166   Adn12166 Human TIF
    23   71   100.0   1464   2 AAW42632   Aaw42632 Human tra
    24   71   100.0   1464   5 ABG69021   Abg69021 Human ste

25	71	100.0	1464	5	AAE22565	Aae22565 Human ste
26	71	100.0	1464	8	ADM93126	Adm93126 Human tra
27	71	100.0	1464	8	ADQ95898	Adq95898 T cell ac
28	63	88.7	1463	2	AAW99482	Aaw99482 Murine NC
29	61	85.9	20	7	ADG17850	Adg17850 Binding a
30	59	83.1	20	7	ADG17811	Adg17811 Binding a
31	59	83.1	20	8	ADJ92854	Adj92854 Co-activa
32	59	83.1	22	4	AAE13047	Aae13047 Nuclear c
33	59	83.1	25	3	AAY99870	Aay99870 Human nuc
34	59	83.1	25	3	AAB13526	Aab13526 Farnesoid
35	59	83.1	25	4	AAE12666	Aae12666 Biotinyla
36	59	83.1	25	5	AAU84220	Aau84220 Molecular
37	59	83.1	32	3	AAY58296	Aay58296 Human p16
38	59	83.1	32	3	AAY58299	Aay58299 Human p16
39	59	83.1	32	3	AAY58293	Aay58293 Human p16
40	59	83.1	32	5	AAO20845	Aao20845 p160 coac
41	59	83.1	32	5	AAO20844	Aao20844 p160 coac
42	59	83.1	32	5	AAO20843	Aao20843 p160 coac
43	59	83.1	149	4	AAM17609	Aam17609 Peptide #
44	59	83.1	149	4	ABB36630	Abb36630 Peptide #
45	59	83.1	149	4	AAM30127	Aam30127 Peptide #

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OM protein - protein search, using sw model

Run on: July 12, 2005, 15:09:14 ; Search time 3.09963 Seconds
                                           (without alignments)
                                           337.165 Million cell updates/sec

Title: US-10-600-751-9
Perfect score: 71
Sequence: 1 KENALLRYLLDKDD 14

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                  1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                  2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                  3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                  4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                  5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	71	100.0	25	4	US-09-868-397-3	Sequence 3, Appli
2	71	100.0	1463	4	US-09-445-353E-3	Sequence 3, Appli
3	71	100.0	1463	4	US-09-949-016-11696	Sequence 11696, A
4	71	100.0	1464	3	US-08-891-640-2	Sequence 2, Appli
5	71	100.0	1464	4	US-09-949-016-6738	Sequence 6738, Ap
6	59	83.1	25	4	US-09-868-397-2	Sequence 2, Appli
7	59	83.1	951	4	US-09-125-635-8	Sequence 8, Appli
8	59	83.1	1302	4	US-09-949-016-10852	Sequence 10852, A
9	59	83.1	1402	4	US-09-125-635-12	Sequence 12, Appl
10	59	83.1	1402	4	US-09-445-353E-2	Sequence 2, Appli
11	59	83.1	1420	4	US-09-125-635-4	Sequence 4, Appli
12	58	81.7	48	3	US-08-891-640-5	Sequence 5, Appli
13	54	76.1	14	3	US-09-302-305C-4	Sequence 4, Appli
14	54	76.1	14	3	US-09-302-305C-17	Sequence 17, Appl
15	54	76.1	15	4	US-09-445-353E-6	Sequence 6, Appli
16	54	76.1	1036	3	US-08-891-640-3	Sequence 3, Appli
17	54	76.1	1061	3	US-08-701-154A-5	Sequence 5, Appli
18	54	76.1	1076	4	US-09-949-016-7421	Sequence 7421, Ap
19	45	63.4	9	4	US-09-053-611-6	Sequence 6, Appli
20	45	63.4	9	4	US-08-975-614-8	Sequence 8, Appli
21	45	63.4	10	4	US-08-975-614-9	Sequence 9, Appli
22	45	63.4	11	4	US-08-975-614-10	Sequence 10, Appl
23	44	62.0	388	3	US-09-134-001C-4951	Sequence 4951, Ap
24	41	57.7	663	4	US-09-107-532A-6861	Sequence 6861, Ap
25	40	56.3	295	4	US-09-248-796A-17141	Sequence 17141, A
26	39	54.9	8	3	US-09-419-826-39	Sequence 39, Appl

27	39	54.9	8	4	US-08-975-614-3	Sequence 3, Appli
28	39	54.9	219	4	US-09-614-912-182	Sequence 182, App
29	39	54.9	427	4	US-09-248-796A-17203	Sequence 17203, A
30	38	53.5	15	4	US-09-053-611-33	Sequence 33, Appl
31	37	52.1	67	4	US-09-248-796A-24749	Sequence 24749, A
32	37	52.1	226	4	US-09-248-796A-19244	Sequence 19244, A
33	37	52.1	232	4	US-09-248-796A-16863	Sequence 16863, A
34	37	52.1	283	4	US-09-602-777A-20	Sequence 20, Appl
35	37	52.1	367	4	US-09-270-767-39016	Sequence 39016, A
36	37	52.1	367	4	US-09-270-767-54233	Sequence 54233, A
37	37	52.1	601	4	US-09-902-540-11184	Sequence 11184, A
38	37	52.1	2781	4	US-09-698-295-10	Sequence 10, Appl
39	37	52.1	2907	4	US-09-698-295-1	Sequence 1, Appli
40	36.5	51.4	114	4	US-09-248-796A-20576	Sequence 20576, A
41	36	50.7	303	4	US-09-248-796A-20412	Sequence 20412, A
42	36	50.7	316	4	US-09-543-681A-4590	Sequence 4590, Ap
43	36	50.7	379	4	US-09-134-000C-4846	Sequence 4846, Ap
44	36	50.7	495	4	US-09-252-991A-20739	Sequence 20739, A
45	36	50.7	505	4	US-09-949-016-6704	Sequence 6704, Ap

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OM protein - protein search, using sw model

Run on: July 12, 2005, 15:16:10 ; Search time 11.1587 Seconds
                                          (without alignments)
                                          484.703 Million cell updates/sec

Title: US-10-600-751-9
Perfect score: 71
Sequence: 1 KENALLRYLLDKDD 14

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 1726218 seqs, 386331768 residues

Total number of hits satisfying chosen parameters: 1726218

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
                 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
                 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep:*
                 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
                 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
                 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	71	100.0	19	15	US-10-346-162-242	Sequence 242, App
2	71	100.0	20	15	US-10-414-692-52	Sequence 52, Appl
3	71	100.0	20	15	US-10-414-583-10	Sequence 10, Appl
4	71	100.0	25	9	US-09-821-984-29	Sequence 29, Appl
5	71	100.0	25	15	US-10-637-190-3	Sequence 3, Appli
6	71	100.0	31	9	US-09-281-717-7	Sequence 7, Appli
7	71	100.0	31	9	US-09-281-717-10	Sequence 10, Appl
8	71	100.0	31	9	US-09-281-717-13	Sequence 13, Appl
9	71	100.0	1263	14	US-10-170-682-1	Sequence 1, Appli
10	71	100.0	1263	14	US-10-217-141-3	Sequence 3, Appli

11	71	100.0	1263	14	US-10-185-731-3	Sequence 3, Appli
12	71	100.0	1263	14	US-10-185-721-3	Sequence 3, Appli
13	71	100.0	1464	9	US-09-842-256-2	Sequence 2, Appli
14	61	85.9	20	15	US-10-414-583-52	Sequence 52, Appl
15	59	83.1	20	15	US-10-414-692-55	Sequence 55, Appl
16	59	83.1	20	15	US-10-414-583-13	Sequence 13, Appl
17	59	83.1	22	9	US-09-815-156-10	Sequence 10, Appl
18	59	83.1	25	9	US-09-821-984-28	Sequence 28, Appl
19	59	83.1	25	15	US-10-637-190-2	Sequence 2, Appli
20	59	83.1	32	9	US-09-281-717-16	Sequence 16, Appl
21	59	83.1	32	9	US-09-281-717-19	Sequence 19, Appl
22	59	83.1	32	9	US-09-281-717-22	Sequence 22, Appl
23	59	83.1	149	9	US-09-864-761-37262	Sequence 37262, A
24	59	83.1	951	14	US-10-379-616-8	Sequence 8, Appli
25	59	83.1	951	16	US-10-473-127-354	Sequence 354, App
26	59	83.1	1402	14	US-10-379-616-12	Sequence 12, Appl
27	59	83.1	1412	16	US-10-473-127-351	Sequence 351, App
28	59	83.1	1412	16	US-10-473-127-352	Sequence 352, App
29	59	83.1	1412	16	US-10-473-127-356	Sequence 356, App
30	59	83.1	1412	16	US-10-473-127-357	Sequence 357, App
31	59	83.1	1415	16	US-10-408-765A-2282	Sequence 2282, Ap
32	59	83.1	1417	16	US-10-473-127-348	Sequence 348, App
33	59	83.1	1417	16	US-10-473-127-359	Sequence 359, App
34	59	83.1	1420	14	US-10-379-616-4	Sequence 4, Appli
35	59	83.1	1420	16	US-10-473-127-349	Sequence 349, App
36	59	83.1	1420	16	US-10-473-127-353	Sequence 353, App
37	59	83.1	1420	16	US-10-473-127-358	Sequence 358, App
38	59	83.1	1424	15	US-10-418-027-1	Sequence 1, Appli
39	59	83.1	1424	16	US-10-473-127-347	Sequence 347, App
40	59	83.1	1424	16	US-10-473-127-350	Sequence 350, App
41	59	83.1	1424	16	US-10-473-127-360	Sequence 360, App
42	59	83.1	1438	16	US-10-333-894A-19	Sequence 19, Appl
43	59	83.1	1522	16	US-10-473-127-355	Sequence 355, App
44	58	81.7	48	9	US-09-842-256-5	Sequence 5, Appli
45	54	76.1	14	9	US-09-953-031A-4	Sequence 4, Appli

OM protein - protein search, using sw model

Run on: July 12, 2005, 15:08:54 ; Search time 2.4797 Seconds
                                          (without alignments)
                                          543.224 Million cell updates/sec

Title: US-10-600-751-9
Perfect score: 71
Sequence: 1 KENALLRYLLDKDD 14

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_79:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	71	100.0	1462	2	T42639	glucocorticoid rec
2	71	100.0	1463	2	T30193	nuclear receptor c
3	59	83.1	1424	2	T03851	thyroid hormone re
4	54	76.1	1061	2	A57620	steroid receptor c
5	43	60.6	229	2	D82230	hypothetical prote
6	42	59.2	99	2	S32700	hypothetical prote
7	42	59.2	261	2	S14882	hypothetical prote
8	42	59.2	342	2	AF2177	glucokinase [impor
9	42	59.2	369	2	T35306	hypothetical prote
10	42	59.2	474	2	T23547	hypothetical prote
11	41	57.7	407	2	H81289	probable sugar tra
12	41	57.7	2262	2	S16664	large protein L -
13	40	56.3	372	2	A64462	8-amino-7-oxononan
14	40	56.3	889	2	T09055	protocadherin 68 -
15	40	56.3	2269	1	JQ1750	genome polyprotein
16	39	54.9	167	2	S73043	hypothetical prote
17	39	54.9	216	2	F90393	phosphoglycerate m
18	39	54.9	364	1	A64729	3-isopropylmalate
19	39	54.9	364	2	E85489	3-isopropylmalate
20	39	54.9	364	2	E90638	3-isopropylmalate
21	39	54.9	389	2	E72761	hypothetical prote
22	39	54.9	420	2	F70842	hypothetical prote
23	39	54.9	423	2	H86996	conserved hypothet
24	39	54.9	582	2	S24545	intermediate filam
25	39	54.9	826	2	F64746	probable membrane
26	39	54.9	2255	1	JQ1532	genome polyprotein
27	38	53.5	218	2	A46143	mu-class glutathio
28	38	53.5	218	2	A23732	glutathione transf

29	38	53.5	268	2	AB1424	E. coli RpiR trans
30	38	53.5	268	2	AH1797	E. coli RpiR trans
31	38	53.5	284	2	AD1141	hypothetical prote
32	38	53.5	284	2	AG1499	hypothetical prote
33	38	53.5	377	2	T40024	probable cytochrom
34	38	53.5	378	2	T18486	hypothetical prote
35	38	53.5	395	2	D87678	thiolase family pr
36	38	53.5	503	2	T51156	calcium dependent
37	38	53.5	546	2	T04336	glutathione syntha
38	38	53.5	623	2	A70741	hypothetical prote
39	38	53.5	841	2	D84513	probable retroelem
40	38	53.5	851	2	H84053	endo-beta-1,3-1,4
41	38	53.5	927	2	T00357	hypothetical prote
42	38	53.5	6359	2	T31679	bacitracin synthet
43	37	52.1	103	2	G42528	B26R protein - vac
44	37	52.1	125	2	B97280	hypothetical prote
45	37	52.1	244	2	T22779	hypothetical prote

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: July 12, 2005, 15:07:23 ; Search time 11.572 Seconds
                                          (without alignments)
                                          619.524 Million cell updates/sec

Title: US-10-600-751-9
Perfect score: 71
Sequence: 1 KENALLRYLLDKDD 14

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   UniProt_03:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

              %
Result   Query
No.   Score Match Length DB ID   Description
----
     1   71 100.0   873 2 Q8BN74   Q8bn74 mus musculu
     2   71 100.0   1393 2 Q7TPU7   Q7tpu7 mus musculu
     3   71 100.0   1462 1 NCO2_MOUSE   Q61026 mus musculu
     4   71 100.0   1464 1 NCO2_HUMAN   Q15596 homo sapien
     5   71 100.0   1465 1 NCO2_RAT   Q9wui9 rattus norv
     6   68 95.8   1505 2 Q98TW1   Q98tw1 brachydanio
     7   66 93.0   1516 1 NCO2_XENLA   Q9w705 xenopus lae
     8   59 83.1   1082 1 NCO3_RAT   Q9epu2 rattus norv
     9   59 83.1   1398 1 NCO3_MOUSE   O09000 m nuclear r
    10   59 83.1   1424 1 NCO3_HUMAN   Q9y6q9 h nuclear r
    11   57 80.3   1391 1 NCO3_XENLA   O57539 xenopus lae
    12   54 76.1   1330 2 Q66JL7   Q66jl7 mus musculu
    13   54 76.1   1441 1 NCO1_HUMAN   Q15788 homo sapien
    14   54 76.1   1447 1 NCO1_MOUSE   P70365 mus musculu
    15   54 76.1   1508 2 Q8UVH3   Q8uvh3 coturnix co
    16   51 71.8   700 2 Q6N6F5   Q6n6f5 rhodopseudo
    17   46 64.8   2271 2 Q8JVA6   Q8jva6 tioman viru
    18   44 62.0   262 2 Q8CPF5   Q8cpf5 staphylococ
    19   44 62.0   1576 2 Q8II47   Q8ii47 plasmodium
    20   43 60.6   229 2 Q9KSR0   Q9ksr0 vibrio chol
    21   43 60.6   262 2 Q73FL8   Q73fl8 wolbachia p
    22   43 60.6   1538 2 Q7QAG9   Q7qag9 anopheles g
    23   42.5 59.9   714 2 Q9LT80   Q9lt80 arabidopsis
    24   42 59.2   261 2 Q04319   Q04319 pichia angu
    25   42 59.2   342 1 GLK_ANASP   P58616 anabaena sp
    26   42 59.2   369 2 Q9S2P6   Q9s2p6 streptomyce
    27   42 59.2   474 2 Q93879   Q93879 caenorhabdi
    28   42 59.2   609 1 DAK_PICAN   O60017 pichia angu
    29   42 59.2   612 2 Q9C2P6   Q9c2p6 neurospora
    30   41 57.7   138 2 Q9T237   Q9t237 phytophthor

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31     41    57.7    287    2   Q6L091              Q6l091 picrophilus
32     41    57.7    407    2   Q9PML7              Q9pml7 campylobact
33     41    57.7    687    2   Q7RB96              Q7rb96 plasmodium
34     41    57.7   1590    2   Q6BJE1              Q6bjel debaryomyce
35     41    57.7   2262    1   RRPL_PI2HT          P26676 human parai
36   40.5    57.0   1877    2   Q6CFU4              Q6cfu4 yarrowia li
37     40    56.3    138    2   Q8N2Z9              Q8n2z9 homo sapien
38     40    56.3    163    2   Q8G4I3              Q8g4i3 bifidobacte
39     40    56.3    184    2   Q7MRQ5              Q7mrq5 wolinella s
40     40    56.3    208    2   Q6C2P1              Q6c2p1 yarrowia li
41     40    56.3    372    1   BIOF_METJA          Q58694 methanococc
42     40    56.3    526    2   Q6JPG3              Q6jpg3 neodiprion
43     40    56.3    709    2   Q8R5Z4              Q8r5z4 fusobacteri
44     40    56.3    761    2   O76733              O76733 drosophila
45     40    56.3    889    1   PC17_HUMAN          O14917 homo sapien
```